

What is claimed is:

1. A method of enhanced biomarker detection using data directed mass filtering comprising the steps of:

selecting an ion trap mass analyzer and an ion filter;

introducing a first separation run of ions from a separation device and ionization source into the ion filter and followed by the ion trap mass analyzer which includes an ion trap and a detector;

accumulating at least a portion of the first separation of ions within the ion trap for an initial period of time for subsequent ion detection by the detector;

measuring mass to charge (m/z) values for a mass spectrum corresponding to desired ion species and undesired ion species contained in the first separation run of ions;

measuring elution times for ions of interest within the first separation run eluted from the separation device to determine a priori retention time intervals for ions of interest;

introducing a second separation run of ions through the separation device and into the ion filter;

measuring elution times for the second separation run of ions to determine whether they fall within at least one a priori determined retention time interval for ions of interest so only ions of interest are filtered and pass from the ion filter into the ion trap to notch out portions of the mass spectrum corresponding to undesired ions; and

accumulating only the ions of interest within the second separation run of ions in the ion trap for a predetermined period of time that is derived at least in part by measured intensities of the ions of interest in the first separation run of ions, and wherein the

predetermined period of time does not exceed a priori retention time intervals for ions of interest determined during the first separation run.

2. The method as recited in claim 1, wherein filtering by the ion filter is disabled during the second separation run when elution times do not fall within at least one a priori retention time interval for ions of interest determined during the first separation run.

3. The method as recited in claim 1, wherein the ion trap mass analyzer includes an automatic gain control (AGC) circuit, and wherein the step of accumulating the desired ions is selectively accomplished with AGC to maintain a desired density of ions within the ion trap.

4. The method as recited in claim 1, wherein the ion filter is a quadrupole linear ion filter.

5. A method of enhanced biomarker detection using data directed mass filtering comprising the steps of:

selecting an ion filter configured in a predetermined arrangement with an ion trap followed by a mass analyzer;

introducing a first separation run of ions from a separation device and ionization source into the ion filter and then through the ion trap followed by the mass analyzer for detection of at least a portion of the first separation run of ions;

measuring mass to charge (m/z) values for a mass spectrum corresponding to desired ion species and undesired ion species contained in the first separation run of ions;

measuring elution times for ions of interest within the first separation run eluted from the separation device to determine a priori determined retention time interval for ions of interest;

introducing a second separation run of ions through the separation device and into the ion filter; and

measuring elution times for the second separation run of ions to determine whether they fall within at least one a priori determined retention time interval for only ions of interest so only ions of interest are filtered and passed from the ion filter onto the ion trap followed by the mass analyzer which provides notching out of portions of the mass spectrum corresponding to undesired ion species.

6. The method as recited in claim 5, wherein only the ions of interest within the second separation run of ions are accumulated in the ion trap for a predetermined period of time that is derived at least in part by measures intensities of the ions of interest from the first separation run of ions, wherein the predetermined period of time does not exceed the selected a priori retention time interval for ions of interest.

7. The method as recited in claim 5, wherein no accumulation of any ions within the second separation run is performed when elution times for the second separation run do not fall within at least one a priori determined retention time interval for the ions of interest to provide broadband acquisition of ions from the second separation run.

8. The method as recited in claim 5, wherein filtering by the ion filter is disabled when elution times for the second separation run do not fall within at least one a priori determined retention time for ions of interest.
9. The method as recited in claim 5, wherein both desired and undesired ions are allowed to pass through the ion filter when elution times for the second separation run of ions do not fall within at least one a priori determined retention time for ions of interest.
10. The method as recited in claim 5, wherein the mass analyzer includes an automatic gain control (AGC) circuit for monitoring intensity information derived from the mass spectrum, and wherein the step of externally accumulating the desired ions is selectively accomplished with AGC to maintain a desired density of ions within the ion trap.
11. The method as recited in claim 5, wherein the mass analyzer is a FTMS device.
12. The method as recited in claim 5, wherein the mass analyzer is a TOF mass analyzer.
13. A method for a-priori biomarker knowledge based mass filtering comprising the following steps of:
 - selecting an ion trap mass analyzer and an ion filter;

eluting an ion sample containing undesired ion species and desired ion species from a separation device that is ionized by an ionization source followed by the ion filter; measuring elution times for the undesired ion species and the desired ion species from the separation device; and filtering out undesired ions with the ion filter by ejecting undesired ion species which fall outside at least one a priori retention time interval corresponding to only desired ion species to provide a tailored biomarker mass spectrum for a predetermined biomarker pattern.

14. The method as recited in claim 13, wherein the tailored biomarker mass spectrum pattern excludes portions corresponding to undesired ion species that are notched-out.